Sig. Frame

Init. Opt.. Length Score Score

0.85

AAAAAAAAAAAAATTCAA X

Optimized Score = 142 Significance = 0.85 Matches = 185 Mismatches = 238 Conservative Substitutions = 0

37 368 83

FastDB

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| 820 | 830 | 840 | 850 | 870 | 870 | 850 | 860 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 
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CACCCAGCCTGCATCCCCAGAACGAAGGAGGGGACATCGCTGTTCCCCCAGAACCCACTATCCTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         880 890 900 910 910 920 930 940 GTTGCTTGCTGCCAGAGAACCTGGGCACTTGCTGCTGATGCCCACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. US-09-886-241-4 (1-1506)
US-09-886-241-3- Sequence 3, Application US/09886241
                                                               1. US-09-886-241-3- Sequence 3, Application U
2. US-09-886-241-5- Sequence 5, Application U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1310 1320 1330
GGCAGAGACCTCTTTGTTGCGTTTTGTGCT
                                 Description
                                                                                                                                                                                                                                                                                                               Initial Score
Residue Identity
                                 Sequence Name
                                                                                                                                                                                                                     Results file 4_x_3_and_5.res made by spaula on Wed 4 Dec 102 14:37:04-PST
                                                                                                                                                                                                                                                                                                                                                                                                                                                Results of the initial comparison of US-09-886-241-4 (1-}505) with:
File : 886241-copy.seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137
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                                                                                                                                                                                                                                                                                                                     Query sequence being compared:US-09-886-241-4 (1-1506)
Number of sequences searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K-tuple
Joining penalty
Window size
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    Fast Pairwise Comparison of Sequences

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Number of scores above cutoff:
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of sequences searched:
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Cap size penalty
Cap size penalty
Cutoff score
Randomization group
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STDEV -9
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A 100% identical sequence to the query sequence was not found. The list of best scores is:

Number o Number o Number o

Times:

Optimized Score = 647 Significance = -0.57 Matches = 825 Mismatches = 621 Conservative Substitutions = 0 2. US-09-886-241-4 (1-1506) US-09-886-241-5- Sequence 5, Application US/09886241 32 47% 300 Initial Score = Residue Identity = Gaps

1290

1260

X 10 TAAATTCCGGCCGCGT-CG 	130 CCATTCCCCTGGCTCAGTCTCC	0 260 TCACCA GA GGAAG 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	310 380 390 CATTG-CTGAGTCTCACCTGCAGTCTAT [11	40 GGCGGAGCTTCCGGAGCTGGGTTA 	510 -AGAAGAG-GAAGAAGAAGG 	560 570 580 TCTGCTGGGCAAAAGACAAC-CTGTGGCCCAGG	640 CCGAGAGATGAGGCTCTGAGUA I 1	700 710 720 730 GGAGGAACTCAGGCCCTTCCCCTTGAGCCTGCAC 111 11 11 11 11 11 11 11 11 11 11 11 11
X	CCTTTGGTTCCCTGAGCCTGAGGGGGGTCCCTGCAGTGCGCTGGCTCAGTCTCCCTGCAGTTGCGCTGGCTCAGTCTCCCTGCAGTTGCGCTGGCTCAGTCTCCTGCAGTTGCGCTGGCTCAGTCTCCTGCAGTTGCGCTGGCTCAGTTATTT	210 250 260 260 260 260 260 260 260 260 260 26	330 340 350 360 360 360 360 360 360 360 360 360 36	400 450 460 460 450 460 450 460 460 450 460 450 460 450 460 450 450 450 450 450 450 450 450 450 45	470 T CCAAGAGAGGAGGAGGAGGAGG - ATGATGA - AGAA GAG GAAGAAGAGGG T CCAAGAGAGGGAGGAGGAGGG - ATGATGA - AGAA GAG - GAAGAAGAGGGG - ATGATGA - AGAA GAG - GAAGAAGAGGGGGGGGGG	\$30 580 580 580 580 580 580 580 580	590 610 620 630 630 640 650	660 670 680 690 700 710 720 730 CCAAGTGGAGCACTAGGGGAGGAACTCAGGCCTTCCCCCTCTGGCCTGCCAC 11 12 20 20 20

AA :	920 930 1 1 1 1 1 1 1 1 1 1	ACA TGA		1070	1140	1200 1210 1220 1230 1240 1250 1250 1250 1250 1250 1250 1250 125	6.1	C GTA	BO IGCAC I AAAA	F - TA
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850 TGCGGCTTCTGACT 	30 C.T.	80 - AG - AG	A – A	19	A A	GA T	06	7-1	3 - 3 -	70 A
85 TT 1 1 06	92 AC 7G	69 - 94 00	AC - AC 70	10 11	A = 8G	AA 80	G- G	9 S	£ - £	T- 17
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830 CCCTCG··CCTGCT 	880 GTCTGTGTTTGCTTGTTTGCCCACCTTTGGCT	AG 0	AC.	00 – p	1 TA	CT PATO	00 1270 1300 1300 1300 1300 1300 1300 1300 13	1340TTGTGCTTTGATG-	1350	41 16 16 75 75
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810 CCTGTTT -CTCTTA	tr tr. 0	0 – 5 –	A = 10	og TT	00-0	F - F	CC	A A A	 16	30-00
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